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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Mon Oct 01 18:08:24 EDT 2007

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Application No: 10566944 Version No: 1.0

**Input Set:****Output Set:**

**Started:** 2007-09-14 12:26:12.517  
**Finished:** 2007-09-14 12:26:29.678  
**Elapsed:** 0 hr(s) 0 min(s) 17 sec(s) 161 ms  
**Total Warnings:** 108  
**Total Errors:** 281  
**No. of SeqIDs Defined:** 192  
**Actual SeqID Count:** 192

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 300	Invalid codon found Ile SEQID (1) POS: 97
E 300	Invalid codon found Glu SEQID (1) POS: 100
E 300	Invalid codon found Asn SEQID (1) POS: 103
E 300	Invalid codon found Tyr SEQID (1) POS: 106
E 300	Invalid codon found Gln SEQID (1) POS: 109
E 300	Invalid codon found Gly SEQID (1) POS: 112
E 300	Invalid codon found Arg SEQID (1) POS: 115
E 300	Invalid codon found Asp SEQID (1) POS: 118
E 300	Invalid codon found Ala SEQID (1) POS: 121
E 300	Invalid codon found Thr SEQID (1) POS: 124
E 300	Invalid codon found Asp SEQID (1) POS: 127
E 300	Invalid codon found Ala SEQID (1) POS: 130
E 300	Invalid codon found Phe SEQID (1) POS: 133
E 300	Invalid codon found Met SEQID (1) POS: 136
E 300	Invalid codon found Val SEQID (1) POS: 139
E 300	Invalid codon found Met SEQID (1) POS: 142
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)

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Error code	Error Description
E 300	Invalid codon found Leu SEQID (1) POS: 481
E 300	Invalid codon found Val SEQID (1) POS: 484
E 300	Invalid codon found Gly SEQID (1) POS: 487
E 300	Invalid codon found Leu SEQID (1) POS: 490 This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

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Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)

**Input Set:****Output Set:**

**Started:** 2007-09-14 12:26:12.517  
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**Total Errors:** 281  
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**Actual SeqID Count:** 192

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (41)
W 402	Undefined organism found in <213> in SEQ ID (42)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (42)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (46)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (58)
W 402	Undefined organism found in <213> in SEQ ID (67)
W 402	Undefined organism found in <213> in SEQ ID (68)
W 402	Undefined organism found in <213> in SEQ ID (69)
W 402	Undefined organism found in <213> in SEQ ID (70)
W 402	Undefined organism found in <213> in SEQ ID (71)
W 402	Undefined organism found in <213> in SEQ ID (72)
W 402	Undefined organism found in <213> in SEQ ID (73)
W 402	Undefined organism found in <213> in SEQ ID (74) This error has occurred more than 20 times, will not be displayed

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**Output Set:**

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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (115)
W 213	Artificial or Unknown found in <213> in SEQ ID (116)
W 213	Artificial or Unknown found in <213> in SEQ ID (121)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (121)
W 213	Artificial or Unknown found in <213> in SEQ ID (122)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (122)
W 213	Artificial or Unknown found in <213> in SEQ ID (123)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (123)
W 213	Artificial or Unknown found in <213> in SEQ ID (124)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (124)
W 213	Artificial or Unknown found in <213> in SEQ ID (125)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (125)
W 213	Artificial or Unknown found in <213> in SEQ ID (126)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (126)
W 213	Artificial or Unknown found in <213> in SEQ ID (127)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (127)
W 213	Artificial or Unknown found in <213> in SEQ ID (128)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (128)
W 213	Artificial or Unknown found in <213> in SEQ ID (129)

**Input Set:**

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Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (129)
W 213	Artificial or Unknown found in <213> in SEQ ID (130)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (130)
W 213	Artificial or Unknown found in <213> in SEQ ID (139)
W 213	Artificial or Unknown found in <213> in SEQ ID (140)
W 213	Artificial or Unknown found in <213> in SEQ ID (141)
W 213	Artificial or Unknown found in <213> in SEQ ID (142)
W 213	Artificial or Unknown found in <213> in SEQ ID (143)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (143)
W 213	Artificial or Unknown found in <213> in SEQ ID (144)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (144)
W 213	Artificial or Unknown found in <213> in SEQ ID (145)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (145)
W 213	Artificial or Unknown found in <213> in SEQ ID (146) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (146)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (147)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (148)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (149)

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Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (150)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (151)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (152) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Zank, Thorsten  
Bauer, Jorg  
Cirpus, Petra  
Abbadie, Amine  
Heinz, Ernst  
Qiu, Xiao  
Vrinten, Patricia  
Sperling, Petra  
Domergue, Frederic  
Meyer, Astrid  
Kirsch, Jelena

<120> METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY ACIDS IN  
TRANSGENIC ORGANISMS

<130> 12810-00193-US

<140> 10566944  
<141> 2007-09-14

<150> DE 103 35 992.3  
<151> 2003-08-01

<150> DE 103 44 557.9  
<151> 2003-09-24

<150> DE 103 47 869.8  
<151> 2003-10-10

<150> DE 103 59 593.7  
<151> 2003-12-18

<150> DE 10 2004 009 457.8  
<151> 2004-02-27

<150> DE 10 2004 012 370.5  
<151> 2004-03-13

<150> DE 10 2004 024 014.0  
<151> 2004-05-14

<160> 192

<170> PatentIn version 3.1

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<212> DNA  
<213> Euglena gracilis

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<221> CDS  
<222> (1)..(1266)

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Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr			
1	5	10	15
tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att			96
Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile			
20	25	30	
ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg			144
Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met			
35	40	45	
cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat			192
His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn			
50	55	60	
ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag			240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu			
65	70	75	80
gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat			288
Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp			
85	90	95	
gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt			336
Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu			
100	105	110	
gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att			384
Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile			
115	120	125	
ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct			432
Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser			
130	135	140	
cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac			480
His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn			
145	150	155	160
ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca			528
Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr			
165	170	175	
tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa			576
Cys Trp Lys Asp Arg His Asn Ala His Ser Ala Thr Asn Val Gln			
180	185	190	
ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag			624
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu			
195	200	205	

gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc 672  
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe  
210 215 220

cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg 720  
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp  
225 230 235 240

tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac 768  
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn  
245 250 255

caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg 816  
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu  
260 265 270

cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc 864  
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile  
275 280 285

ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc 912  
Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe  
290 295 300

ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc 960  
Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile  
305 310 315 320

ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat 1008  
Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His  
325 330 335

gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga 1056  
Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly  
340 345 350

ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc 1104  
Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg  
355 360 365

cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag 1152  
His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys  
370 375 380

cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc 1200  
His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile  
385 390 395 400

ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc 1248  
Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro  
405 410 415

gcg ggg aag gct cta taa 1266  
Ala Gly Lys Ala Leu

<210> 2  
<211> 421  
<212> PRT  
<213> Euglena gracilis

<400> 2

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr  
1 5 10 15

Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile  
20 25 30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met  
35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn  
50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu  
65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp  
85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu  
100 105 110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile  
115 120 125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser  
130 135 140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn  
145 150 155 160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr  
165 170 175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln  
180 185 190

Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu  
195 200 205

Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe  
210 215 220

Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp  
225 230 235 240

Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn  
245 250 255

Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu  
260 265 270

His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile  
275 280 285

Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe  
290 295 300

Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile  
305 310 315 320

Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His  
325 330 335

Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly  
340 345 350

Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg  
355 360 365

His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys  
370 375 380

His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile  
385 390 395 400

Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro  
405 410 415

Ala Gly Lys Ala Leu

420

<210> 3

<211> 777

<212> DNA

<213> Isochrysis galbana

<220>

<221> CDS

<222> (1)...(777)

<223> delta9-elongase

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atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc 48  
Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr  
1 5 10 15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96  
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Lys Pro  
20 25 30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144  
Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg  
35 40 45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192  
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu  
50 55 60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240  
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly  
65 70 75 80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288  
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln  
85 90 95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336  
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys  
100 105 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg 384  
Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu  
115 120 125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat 432  
Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp  
130 135 140

gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg 480  
Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met  
145 150 155 160

ttt ttc aac tcc ttc att cac acc atc atg tac acc tac tac ggc ctc 528  
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Gly Leu

	165	170	175	
acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met				576
180	185	190		
cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile				624
195	200	205		
aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala				672
210	215	220		
ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe				720
225	230	235	240	
ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys				768
245	250	255		
cag ctc tag Gln Leu				777

<210> 4  
<211> 258  
<212> PRT  
<213> Isochrysis galbana

<400> 4

Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr			
1	5	10	15

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro			
20	25	30	

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg			
35	40	45	

Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu			
50	55	60	

Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly			
65	70	75	80

Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln			
85	90	95	

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys  
100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu  
115 120 125

Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp  
130 135 140

Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met  
145 150 155 160

Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu  
165 170 175

Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met  
180 185 190

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Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
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